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  1 GAATTTGGCC CTCGAGGCCA AGAATTCGGC ACGAGGCGCG GCGCCCAGCG CAGGCAGAGC GCTGTCGCAT CCCGGGCGTC CACCCGCCAT GGGGCTCTCC
    CTTAAACCGG GAGCTCCGGT TCTTAAGCCG TGCTCCGCGC CGCGGGTCGC GTCCGTCTCG CGACAGCGTA GGGCCCGCAG GTGGGCGGTA CCCCGAGAGG
  1                                                                                                        Me tGlyLeuSer

101 TGGAGCCCGC GACCTCCACT GCTGATGATC CTGCTACTGG TGCTGTCGTT GTGGCTGCCA CTTGGAGCAG GAAACTCCCT TGCCACAGAG AACAGGTTTG
    ACCTCGGGCG CTGGAGGTGA CGACTACTAG GACGATGACC ACGACAGCAA CACCGACGGT GAACCTCGTC CTTTGAGGGA ACGGTGTCTC TTGTCCAAAC
  5 TrpSerProA rgProProLe uLeuMetIle LeuLeuLeuV alLeuSerLe uTrpLeuPro LeuGlyAlaG lyAsnSerLe uAlaThrGlu AsnArgPheVal

201 TGAACAGCTG TACCCAGGCC AGAAAGAAAT GCGAGGCTAA TCCCGCTTGC AAGGCTGCCT ACCAGCACCT GGGCTCCTGC ACCTCCAGTT TAAGCAGGCC
    ACTTGTCGAC ATGGGTCCGG TCTTTCTTTA CGCTCCGATT AGGGCGAACG TTCCGACGGA TGGTCGTGGA CCCGAGGACG TGGAGGTCAA ATTCGTCCGG
 39   AsnSerCy sThrGlnAla ArgLysLysC ysGluAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe uGlySerCys ThrSerSerL euSerArgPro

301 GCTGCCCTTA GAGGAGTCTG CCATGTCTGC AGACTGCCTA GAGGCAGCAG AACAACTCAG GAACAGCTCT CTGATAGACT GCAGGTGCCA TCGGCGCATG
    CGACGGGAAT CTCCTCAGAC GGTACAGACG TCTGACGGAT CTCCGTCGTC TTGTTGAGTC CTTGTCGAGA GACTATCTGA CGTCCACGGT AGCCGCGTAC
 72  LeuProLeu GluGluSerA laMetSerAl aAspCysLeu GluAlaAlaG luGlnLeuAr gAsnSerSer LeuIleAspC ysArgCysHi sArgArgMet

401 AAGCACCAAG CTACCTGTCT GGACATTTAT TGGACCGTTC ACCCTGCCCG AAGCCTTGGT GACTACGAGT TGGATGTCTC ACCCTATGAA GACACAGTGA
    TTCGTGGTTC GATGGACAGA CCTGTAAATA ACCTGGCAAG TGGGACGGGC TTCGGAACCA CTGATGCTCA ACCTACAGAG TGGGATACTT CTGTGTCACT
105 LysHisGlnA laThrCysLe uAspIleTyr TrpThrValH isProAlaAr gSerLeuGly AspTyrGluL euAspValSe rProTyrGlu AspThrValThr

501 CCAGCAAACC CTGGAAAATG AATCTTAGCA AGTTGAACAT GCTCAAACCA GACTCGGACC TCTGCCTCAA ATTTGCTATG CTGTGTACTC TTCACGACAA
    GGTCGTTTGG GACCTTTTAC TTAGAATCGT TCAACTTGTA CGAGTTTGGT CTGAGCCTGG AGACGGAGTT TAAACGATAC GACACATGAG AAGTGCTGTT
139   SerLysPr oTrpLysMet AsnLeuSerL ysLeuAsnMe tLeuLysPro AspSerAspL euCysLeuLy sPheAlaMet LeuCysThrL euHisAspLys

601 GTGTGACCGC CTGCGCAAGG CCTACGGGGA GGCATGCTCA GGGATCCGCT GCCAGCGCCA CCTCTGCCTA GCCCAGCTGC GCTCCTTCTT TGAGAAGGCA
    CACACTGGCG GACGCGTTCC GGATGCCCCT CCGTACGAGT CCCTAGGCGA CGGTCGCGGT GGAGACGGAT CGGGTCGACG CGAGGAAGAA ACTCTTCCGT
172  CysAspArg LeuArgLysA laTyrGlyGl uAlaCysSer GlyIleArgC ysGlnArgHi sLeuCysLeu AlaGlnLeuA rgSerPhePh eGluLysAla

701 GCAGAGTCCC ACGCTCAGGG TCTGCTGCTG TGTCCCTGTG CACCAGAAGA TGCGGGCTGT GGGGAGCGGC GGCGTAACAC CATCGCCCCC AGTTGCGCCC
    CGTCTCAGGG TGCGAGTCCC AGACGACGAC ACAGGGACAC GTGGTCTTCT ACGCCCGACA CCCCTCGCCG CCGCATTGTG GTAGCGGGGG TCAACGCGGG
205 AlaGluSerH isAlaGlnGl yLeuLeuLeu CysProCysA laProGluAs pAlaGlyCys GlyGluArgA rgArgAsnTh rIleAlaPro SerCysAlaLeu

801 TGCCTTCTGT AACCCCCAAT TGCCTGGATC TGCGGAGCTT CTGCCGTGCG GACCCTTTGT GCAGATCACG CCTGATGGAC TTCCAGACCC ACTGTCATCC
    ACGGAAGACA TTGGGGGTTA ACGGACCTAG ACGCCTCGAA GACGGCACGC CTGGGAAACA CGTCTAGTGC GGACTACCTG AAGGTCTGGG TGACAGTAGG
239   ProSerVa lThrProAsn CysLeuAspL euArgSerPh eCysArgAla AspProLeuC ysArgSerAr gLeuMetAsp PheGlnThrH isCysHisPro

901 TATGGACATC CTTGGGACTT GTGCAACTGA GCAGTCCAGA TGTCTGCGGG CATACCTGGG GCTGATTGGG ACTGCCATGA CCCCAAACTT CATCAGCAAG
    ATACCTGTAG GAACCCTGAA CACGTTGACT CGTCAGGTCT ACAGACGCCC GTATGGACCC CGACTAACCC TGACGGTACT GGGGTTTGAA GTAGTCGTTC
272  MetAspIle LeuGlyThrC ysAlaThrGl uGlnSerArg CysLeuArgA laTyrLeuGl yLeuIleGly ThrAlaMetT hrProAsnPh eIleSerLys
```

FIG. 1A

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1001 GTCAACACTA CTGTTGCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGGAAAGGTC CTTCTCCCAG AACCCCTGCC
     CAGTTGTGAT GACAACGGAA TTCGACGTGG ACGGCTCCGT CGCCGTTGGA TGTCCTGCTC ACACTTGTCG ACCTTTCCAG GAAGAGGGTC TTGGGGACGG
 305 ValAsnThrT hrValAlaLe uSerCysThr CysArgGlyS erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu

1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
     AGCACCTCCG GTAACGTCGA TTCTACGCAA AGGTGTCTGT CGAGAAGAGG GTCCTGACCC GTCTGAGATG AAAAAGTCAC CACGTCGTCG TCTTGTCGTT
 339   ValGluAl aIleAlaAla LysMetArgP heHisArgGl nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG lnAsnSerAsn

1201 CCCTGCTCTG AGACTGCAGC CCAGGCTACC CATTCTTTCT TTCTCCATCC TTCCCTTGAT TCTGCTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
     GGGACGAGAC TCTGACGTCG GGTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGGAACTA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
 372  ProAlaLeu ArgLeuGlnP roArgLeuPr oIleLeuSer PheSerIleL euProLeuIl eLeuLeuGln ThrLeuTrp

1301 CTTTGTCCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA GAAGACGCAG CGTGCTACAC AGCAACCCGG
     GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCCTCT CTTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC

1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAACC
     TTGGTTGGTC CGTAAGGCGT CGTGTAGGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG

1501 TCCCTTGCCC CTGCTTCCTT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTGCCTTC TGTTCTGATG GTGATTAGCG GCTCACCTCC
     AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAAACGGAAG ACAAGACTAC CACTAATCGC CGAGTGGAGG

1601 AGCGCTTCTT CCTGTTTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGGTGACTG
     TCGCGAAGAA GGACAAAGGG TCCTGGTGGG TCTCCGATTC CTTAGTCAGT AAGGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCCAAGA CTCCACTGAC

1701 AGAAAAATGT TTCCTTTGTG TGGAAGGCTG GTGCTCCAGC CTCCACGTCC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
     TCTTTTTACA AAGGAAACAC ACCTTCCGAC CACGAGGTCG GAGGTGCAGG GAGACTTACC TTCTATTTTT GGACGACCAC AGAACTGACG AGACGGTCCG

1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTTTAA CTCCTATTAC TGTCCCCAAA TTCCCCTAGT CCCTTGGGTC ATGATTAAAC
     TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGGTTT AAGGGGATCA GGGAACCCAG TACTAATTTG

1901 ATTTTGACTT AAAAAAAAAA AAAAAAAAAA AAAAA
     TAAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTT
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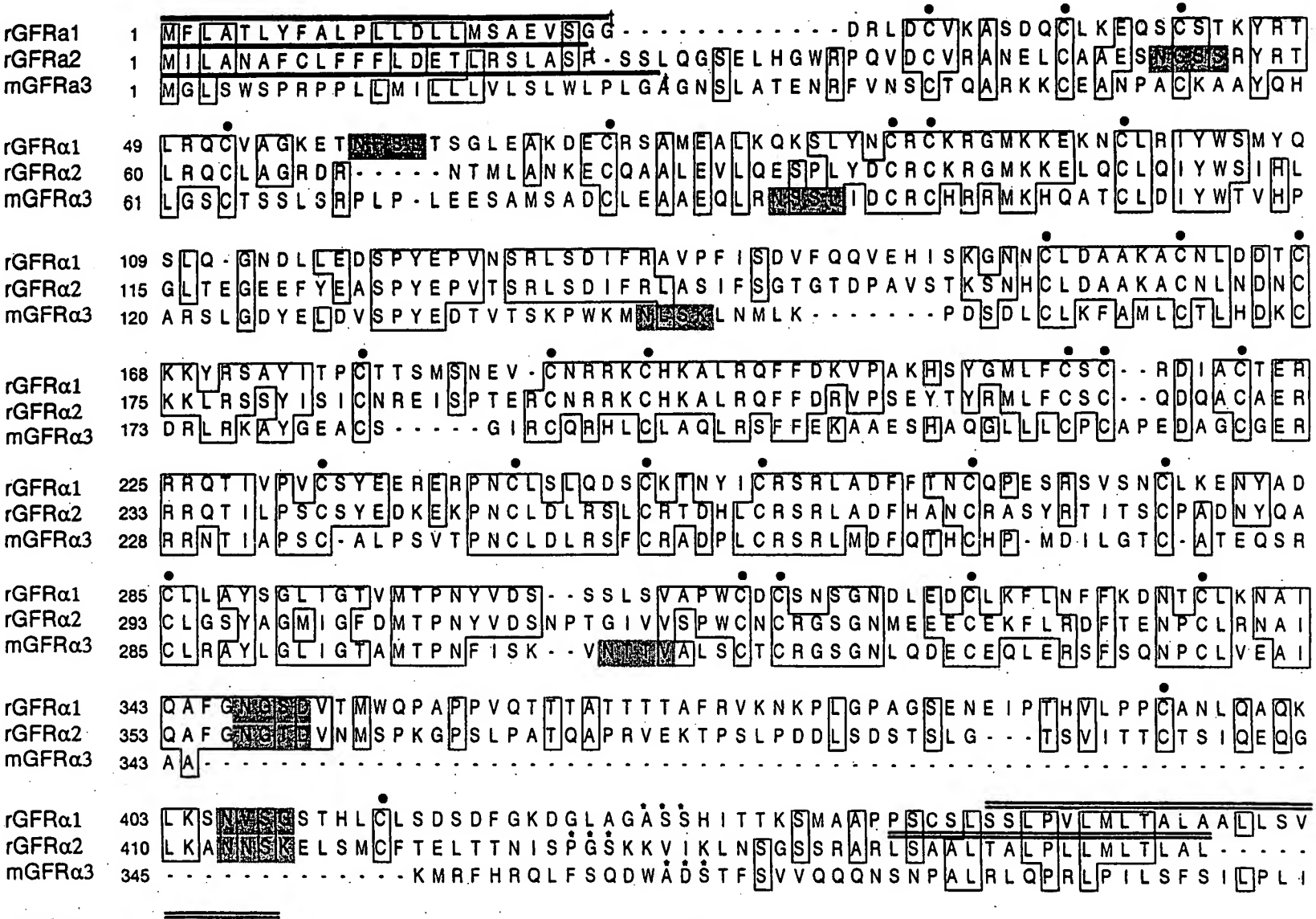
FIG. 1B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mGFRa3 1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH
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rGFRα2 60 LRQCLAGRDR-----NTMLANKECQAAALEVLQESPLYDCRCKRGMKKELQCLQIYWSIFL
mGFRα3 61 LGSCTSSLSRPLP-LEESAMSADCLEAAEQLRNSSSQIDCRCHRRMKHQATCLDIYWTVHP
rGFRα1 109 SLQ-GNDLLEDSPYEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTC
rGFRα2 115 GLTEGEEFYEASPYEPVTSRLSDIFRLASIFSGTGTDPAVSTKSNHCLDAAKACNLNDNC
mGFRα3 120 ARSLGDYELDVSPYEDTVTSKPWKMNESKLNMLK-------PDSDLCLKFAMLCTLHDKC
rGFRα1 168 KKYRSAYITPCTTSMSNEV-CNRRKCHKALRQFFDKVPAKHSYGMLFCSC--RDIACTER
rGFRα2 175 KKLRSSYISICNREISPTERCNRRKCHKALRQFFDRVPSEYTYRMLFCSC--QDQACAER
mGFRα3 173 DRLRKAYGEACS-----GIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGER
rGFRα1 225 RRQTIVPVCSYEERERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYAD
rGFRα2 233 RRQTILPSCSYEDKEKPNCLDLRSLCRTDHLCRSRLADFHANCRASYRTITSCPADNYQA
mGFRα3 228 RRNTIAPSC-ALPSVTPNCLDLRSFCRADPLCRSRLMDFQTHCHP-MDILGTC-ATEQSR
rGFRα1 285 CLLAYSGLIGTVMTPNYVDS--SSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAI
rGFRα2 293 CLGSYAGMIGFDMTPNYVDSNPTGIVVSPWCNCRGSGNMEEECEKFLRDFTENPCLRNAI
mGFRα3 285 CLRAYLGLIGTAMTPNFISK--VNLTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAI
rGFRα1 343 QAFGNGSDVTMWQPAPPVQTTTATTTTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQK
rGFRα2 353 QAFGNGTDVNMSPKGPSLPATQAPRVEKTPSLPDDLSDSTSLG---TSVITTCTSIQEQG
mGFRα3 343 AA----------
rGFRα1 403 LKSNWSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSV
rGFRα2 410 LKANNSKELSMCFTELTTNISPGSKKVIKLNSGSSRARLSAALTALPLLMLTLAL-----
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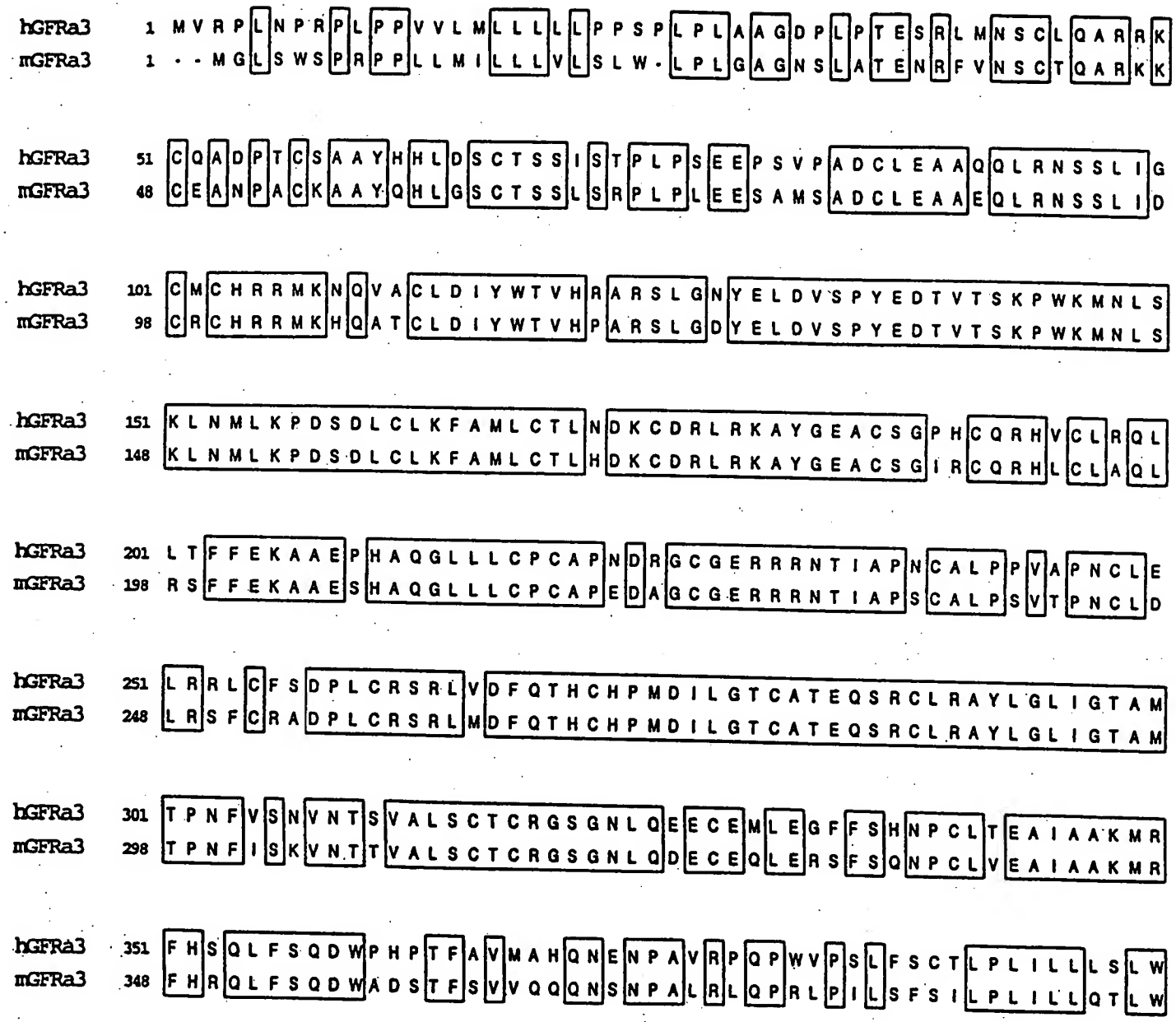
mGFRα3 392 LLQTLW

FIG. 2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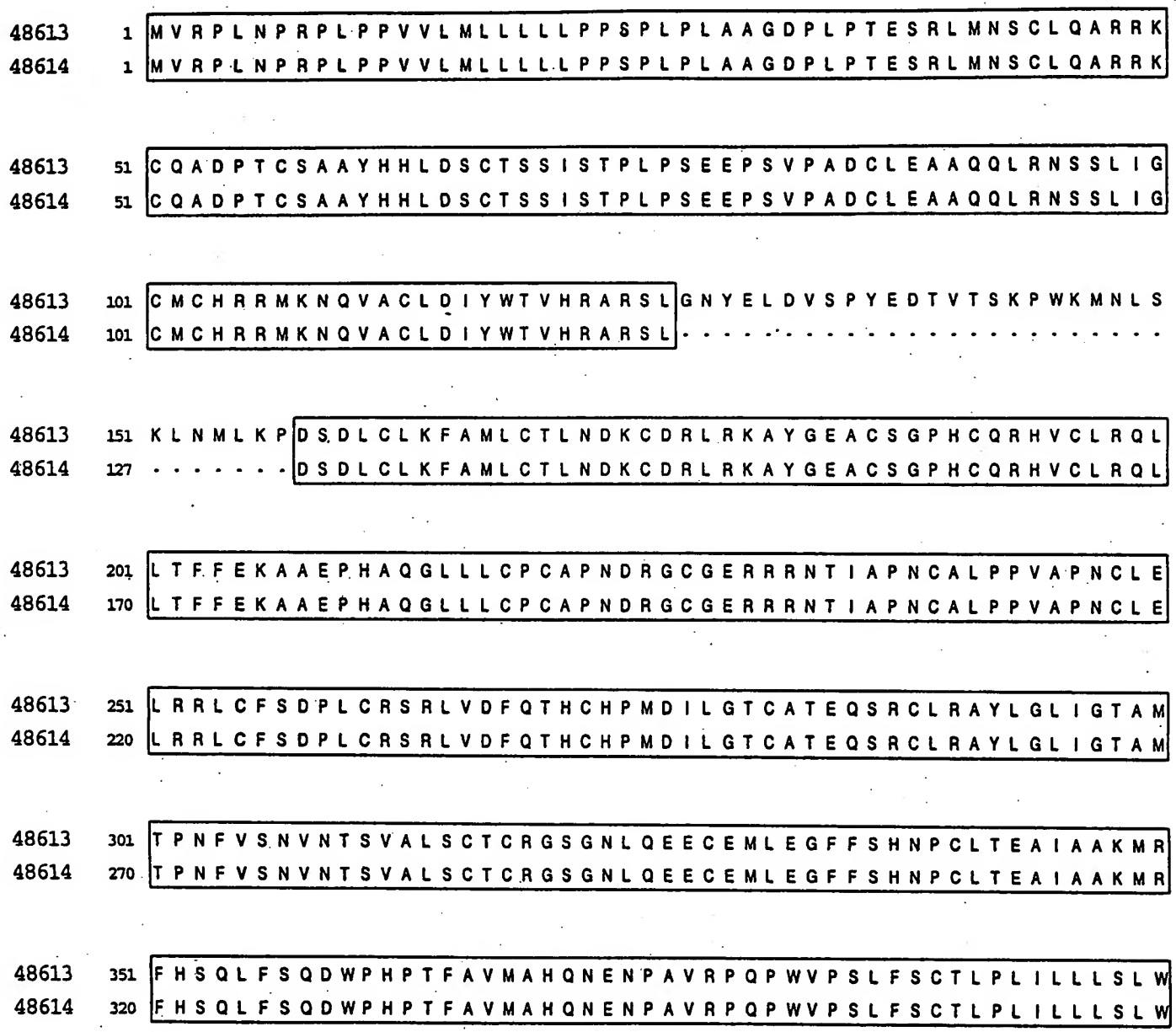
mGFRa3 1 --MGLSWSPRPPLLMILLLVLSLW-LPLGAAGNSLATENRFVNSCTQARKK
hGFRa3 51 CQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
mGFRa3 48 CEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLID
hGFRa3 101 CMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTVTSKPWKMNLS
mGFRa3 98 CRCHRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLS
hGFRa3 151 KLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
mGFRa3 148 KLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQL
hGFRa3 201 LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
mGFRa3 198 RSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD
hGFRa3 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
mGFRa3 248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
hGFRa3 301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
mGFRa3 298 TPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMR
hGFRa3 351 FHSQLFSQDWPHPTFAVMAHQNENPAVRPQPWVPSLFSCTLPLILLLSLW
mGFRa3 348 FHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW

FIG. 3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48614 220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
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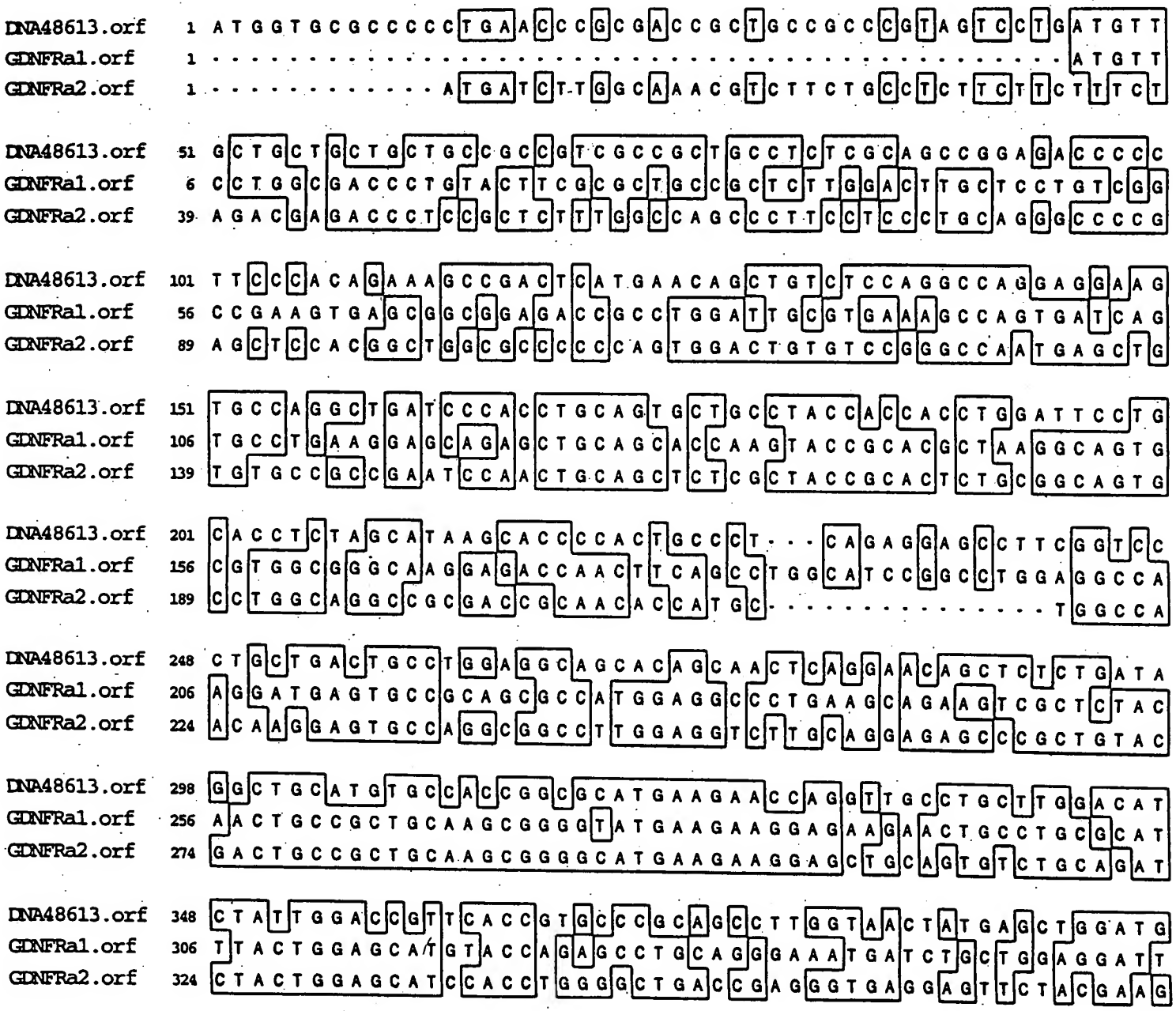
48614 270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48613 351 FHSQLFSQDWPHPTFAVMAHQNENPAVRPQPWVPSLFSCTLPLILLLSLW
48614 320 FHSQLFSQDWPHPTFAVMAHQNENPAVRPQPWVPSLFSCTLPLILLLSLW

FIG. 4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GDNFRa1.orf 1 ATGTT
GDNFRa2.orf 1 ATGATCTTGGCAAACGTCTTCTGCCTCTTCTTCTTTCT
DNA48613.orf 51 GCTGCTGCTGCTGCCGCCGTCGCCGCTGCCTCTCGCAGCCGGAGACCCCC
GDNFRa1.orf 6 CCTGGCGACCCTGTACTTCGCGCTGCCGCTCTTGGACTTGCTCCTGTCGG
GDNFRa2.orf 39 AGACGAGACCCTCCGCTCTTGGCCAGCCTTCCTCCCTGCAGGGCCCCG
DNA48613.orf 101 TTCCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAG
GDNFRa1.orf 56 CCGAAGTGAGCGGCGGAGACCGCCTGGATTGCGTGAAAGCCAGTGATCAG
GDNFRa2.orf 89 AGCTCCACGGCTGGCGCCCCCAGTGGACTGTGTCCGGGCCAATGAGCTG
DNA48613.orf 151 TGCCAGGCTGATCCCACCTGCAGTGCTGCCTACCACCACCTGGATTCCTG
GDNFRa1.orf 106 TGCCTGAAGGAGCAGAGCTGCAGCACCAAGTACCGCACGCTAAGGCAGTG
GDNFRa2.orf 139 TGTGCCGCCGAATCCAACTGCAGCTCTCGCTACCGCACTCTGCGGCAGTG
DNA48613.orf 201 CACCTCTAGCATAAGCACCCCACTGCCCT---CAGAGGAGCCTTCGGTCC
GDNFRa1.orf 156 CGTGGCGGGCAAGGAGACCAACTTCAGCCTGGCATCCGGCCTGGAGGCCA
GDNFRa2.orf 189 CCTGGCAGGCCGCGACGCAACACCATGC----------TGGCCA
DNA48613.orf 248 CTGCTGACTGCCTGGAGGCAGCACAGCAACTCAGGAACAGCTCTCTGATA
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DNA48613.orf 298 GGCTGCATGTGCCACCGGCGCATGAAGAACCAGGTTGCCTGCTTGGACAT
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GDNFRa2.orf 324 CTACTGGAGCATCCACCTGGGGCTGACCGAGGGTGAGGAGTTCTACGAAG

FIG. 5A

DNA48613.orf 398 TCTCCCCCTATGAAG.....ACACAGTGACCAGC
GDNFRa1.orf 356 CCCCATATGAACCAGTTA.....ACAGCAGATTGTCA
GDNFRa2.orf 374 CCTCCCCCTATGAGCCGGTGACCTCCCGCCTCTCGGACATCTTCAGGCTT
DNA48613.orf 427 AAACCCTGGAAAATGAATCTCAGCAAACTGAACATGCTCAAACCAGACTC
GDNFRa1.orf 388 GATATATTCCGGGTGGTCCCATTCATATCAGTGGAGCACATTCCCAAAGG
GDNFRa2.orf 424 GCTTCAATCTTCTCAGGGACAGGGGCAGACCCGGTGGTCAGCGCCAAGAG
DNA48613.orf 477 AGACCTCTGCCTCAAGTTTGCCATGCTGTGTACTCTCAATGACAAGTGTG
GDNFRa1.orf 438 GAACAACTGCCTGGATGCAGCGAAGGCCTGCAAACCTCGACGACATTTGCA
GDNFRa2.orf 474 CAACCATTGCCTGGATGCTGCCAAGGCCTGCAAACCTGAATGACAACTGCA
DNA48613.orf 527 ACCGGCTGCGCAAGGCCTACGGGGAGGCGTGCTCCGGGCCCCACTG---C
GDNFRa1.orf 488 AGAAGTACAGGTCGGCGTACATCACCCCGTGCACCACCAGCGTGTC---C
GDNFRa2.orf 524 AGAAGCTGCGCTCCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCCC
DNA48613.orf 574 CAGCGCCACGTCTGCCTCAGGCAGCTGCTCACTTTCTTCGAGAAGGCCGC
GDNFRa1.orf 535 AATGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTT
GDNFRa2.orf 574 ACCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTT
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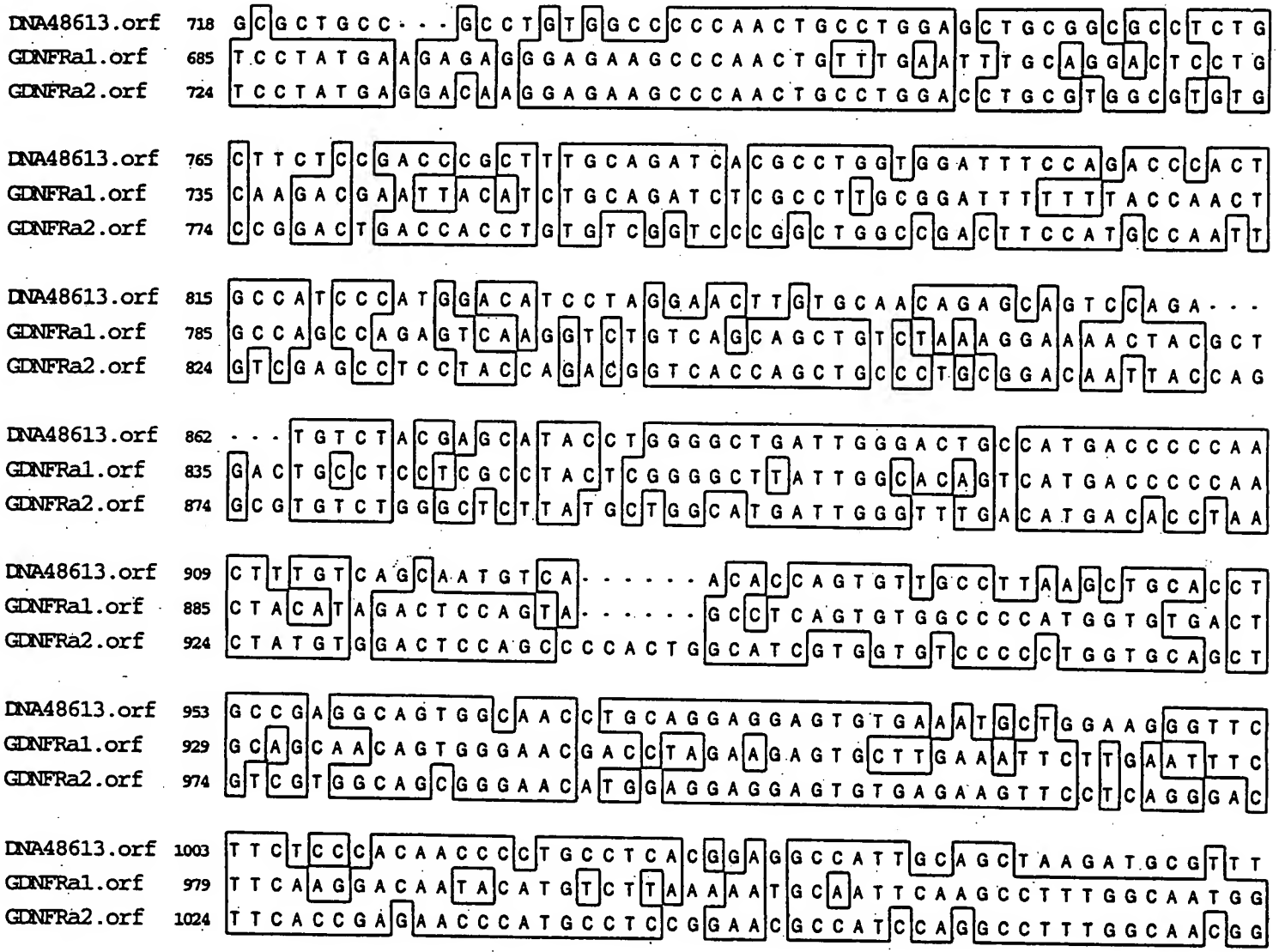
GDNFRa1.orf 585 TGACAAGGTCCCGGCCAAGCACAGCTACGGAATGCTCTTCTGCTCCTGCC
GDNFRa2.orf 624 CGACCGGGTGCCCAGCGAGTACACCTACCGCATGCTCTTCTGCTCCTGCC
DNA48613.orf 668 ACGACCGGGGCTGCGGGGAGCGCCGGCGCAACACCATCGCCCCCAACTGC
GDNFRa1.orf 635 GGGACATCGCCTGCACAGAGCGGAGGCGACAGACCATCGTGCCTGTGTGC
GDNFRa2.orf 674 AAGACCAGGCGTGCGCTGAGCGCCGCCGGCAACACCATCCTGCCCAGCTGC

FIG. 5B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GDNFRa1.orf 735 CAAGACGAATTACATCTGCAGATCTTCGCCTTGCGGATTTTTTACCAACT
GDNFRa2.orf 774 CCGGACTGACCACCTGTGTCGGTCCCGGCTGGCCGACTTCCATGCCAATT
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GDNFRa1.orf 785 GCCAGCCAGAGTCAAGGTCTGTCAGCAGCTGTCTAAAGGAAAACTACGCT
GDNFRa2.orf 824 GTCGAGCCTCCTACCAGACGGTCACCAGCTGCCCTGCGGACAATTACCAG
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GDNFRa1.orf 835 GACTGCCTCCTCGCCTACTCGGGGCTTATTGGCACAGTCATGACCCCCAA
GDNFRa2.orf 874 GCGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAA
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GDNFRa1.orf 885 CTACATAGACTCCAGTA------GCCTCAGTGTGGCCCCATGGTGTGACT
GDNFRa2.orf 924 CTATGTGGACTCCAGCCCCACTGGCATCGTGGTGTCCCCCTGGTGCAGCT
DNA48613.orf 953 GCCGAGGCAGTGGCAACCTGCAGGAGGAGTGTGAAATGCTGGAAGGGTTC
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GDNFRa2.orf 974 GTCGTGGCAGCGGGAACATGGAGGAGGAGTGTGAGAAGTTCCTCAGGGAC
DNA48613.orf 1003 TTCTCCCACAACCCCTGCCTCACGGAGGCCATTGCAGCTAAGATGCGTTT
GDNFRa1.orf 979 TTCAAGGACAATACATGTCTTAAAAATGCAATTCAAGCCTTTGGCAATGG
GDNFRa2.orf 1024 TTCACCGAGAACCCATGCCTCCGGAACGCCATCCAGGCCTTTGGCAACGG

FIG. 5C

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GDNFRa1.orf 1029 CTCCGATGTGACCGTGTGGCAGCCAGCCTTCCCAGTACAGACCACCACTG
GDNFRa2.orf 1074 CACGGACGTGAACGTGTCCCCAAAGGCCCCTCGTTCCAGGCCACCCAGG
DNA48613.orf 1103 TGGCACACCAGAATGAAACCCTGCTGTGAGGCCACAGCCCTGGGGTGCCC
GDNFRa1.orf 1079 CCACTACCACCACTGCCCTCCGGGTTAAGAACAACCCCTGGGGCCAGCA
GDNFRa2.orf 1124 CCCCTCGGGTGGAGAAGACGCCTTCTTTGCCAGATGACCTCAGTGACAGT
DNA48613.orf 1153 TCTCTTTTCTCCTGCACGCTTCCCTTGATTCTGCTCCTGAGCCTATGGTA
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GDNFRa2.orf 1174 ACCAGCTTGGGGACCAGTGTCATCACCACCTGCACGTCTGTCCAGGAGCA
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GDNFRa1.orf 1179 ACAGGCACAGAAGCTGAAATCCAATGTGTCGGGCAATACACACCTCTGTA
GDNFRa2.orf 1224 GGGGCTGAAGGCCAACAACTCCAAAGAGTTAAGCATGTGCTTCACAGAGC
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GDNFRa2.orf 1274 TCACGACAAATATCATCCCAGGGAGTAACAAGGTGATCAAACCTAACTCA
GDNFRa1.orf 1279 ACCACAAAATCAATGGCTGCTCCTCCAAGCTGTGGTCTGAGCCCACTGCT
GDNFRa2.orf 1324 GGCCCCAGCAGAGCCAGACCGTCGGCTGCCTTGACCGTGCTGTCTGTCCT
GDNFRa1.orf 1329 GGTCCTGGTGGTAACCGCTCTGTCCACCCTATTATCTTTAACAGAAACAT
GDNFRa2.orf 1374 GATGCTGAAACAGGCCTTGTAG
GDNFRa1.orf 1379 CATAG

FIG. 5D

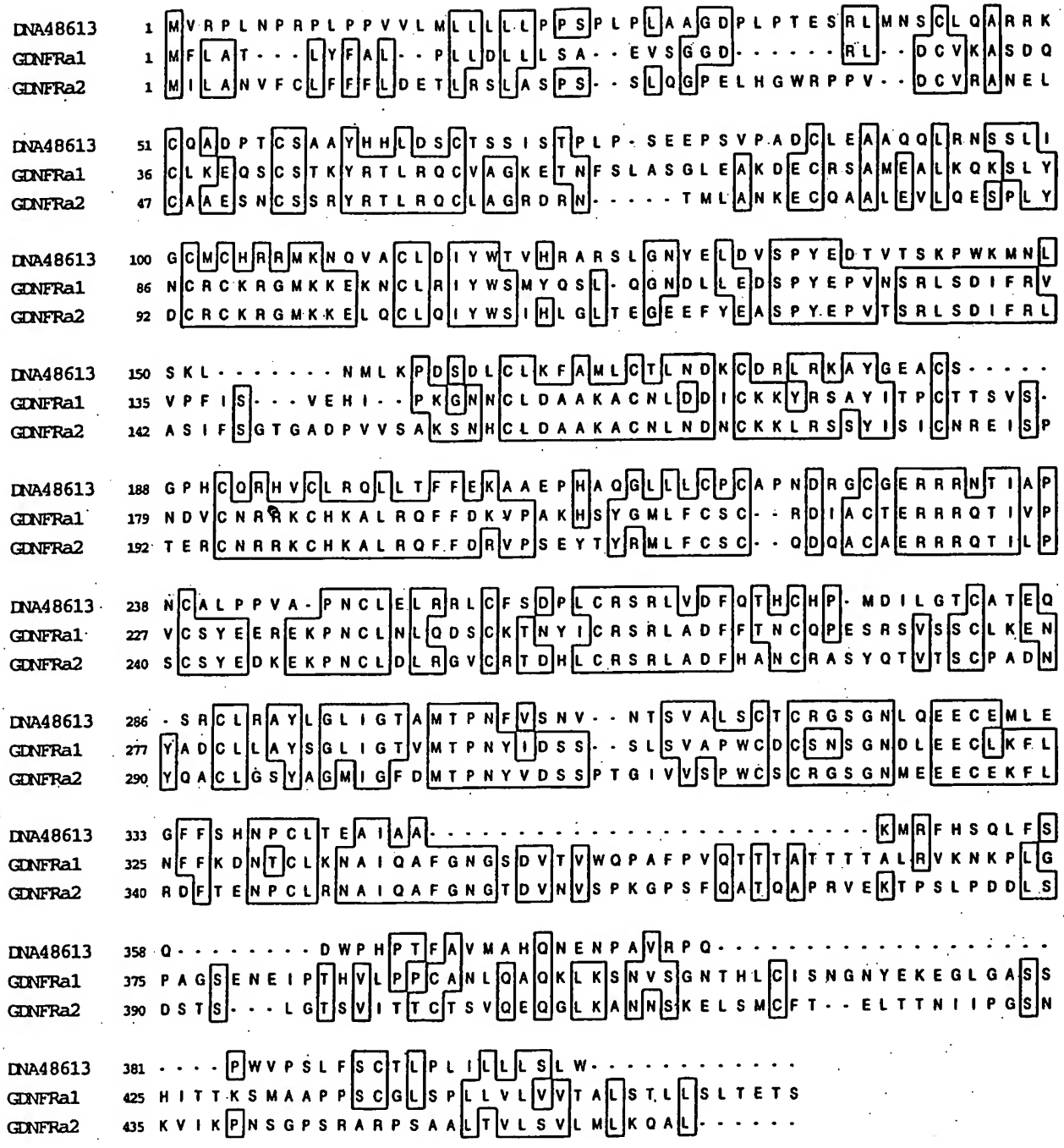

DNA48613 1 MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRK
GDNFRa1 1 MFLAT---LYFALL--PLLDLLLSA--EVSGGD------RL--DCVKASDQ
GDNFRa2 1 MILANVFCLFFFLDETLRSLASPS--SLQGPELHGWRPPV--DCVRANEL
DNA48613 51 CQADPTCSAAYHHLDSCTSSISTPLP-SEEPSVPADCLEAAQQLRNSSLI
GDNFRa1 36 CLKEQSCSTKYRTLRQCVAGKETNFSLASGLEAKDECRSAMEALKQKSLY
GDNFRa2 47 CAAESNCSSRYRTLRQCLAGRDRN----TMLANKECQAALEVLQESPLY
DNA48613 100 GCMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTVTSKPWKMNL
GDNFRa1 86 NCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEPVNSRLSDIFRV
GDNFRa2 92 DCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRL
DNA48613 150 SKL-------NMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACS-----
GDNFRa1 135 VPFIS---VEHI--PKGNNCLDAAKACNLDDICKKYRSAYITPCTTSVS-
GDNFRa2 142 ASIFSGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREISP
DNA48613 188 GPHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAP
GDNFRa1 179 NDVCNRRKCHKALRQFFDKVPAKHSYGMLFCSC--RDIACTERRRQTIVP
GDNFRa2 192 TERCNRRKCHKALRQFFDRVPSEYTYRMLFCSC--QDQACAERRRQTILP
DNA48613 238 NCALPPVA-PNCLELRRLCFSDPLCRSRLVDFQTHCHP-MDILGTCATEQ
GDNFRa1 227 VCSYEERKPNCLNLQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKEN
GDNFRa2 240 SCSYEDKKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADN
DNA48613 286 -SRCLRAYLGLIGTAMTPNFVSNV--NTSVALSCTCRGSGNLQEECEMLE
GDNFRa1 277 YADCLLAYSGLIGTVMTPNYIDSS--SLSVAPWCDCSNSGNDLEECLKFL
GDNFRa2 290 YQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNMEEECEKFL
DNA48613 333 GFFSHNPCLTEAIAA----------KMRFHSQLFS
GDNFRa1 325 NFFKDNTCLKNAIQAFGNGSDVTVWQPAFPVQTTTATTTTALRVKNKPLG
GDNFRa2 340 RDFTENPCLRNAIQAFGNGTDVNVSPKGPSFQATQAPRVEKTPSLPDDLS
DNA48613 358 Q--------DWPHPTFAVMAHQNENPAVRPQ----------
GDNFRa1 375 PAGSENEIPTHVLPPCANLQAQKLKSNVSGNTHLCISNGNYEKEGLGASS
GDNFRa2 390 DSTS---LGTSVITTCTSVQEQGLKANNSKELSMCFT--ELTTNIIPGSN
DNA48613 381 ----PWVPSLFSCTLPLILLLSLW----------
GDNFRa1 425 HITTKSMAAPPSCGLSPLLVLVVTALSTLLSLTETS
GDNFRa2 435 KVIKPNSGPSRARPSAALTVLSVLMLKQAL------

FIG. 6

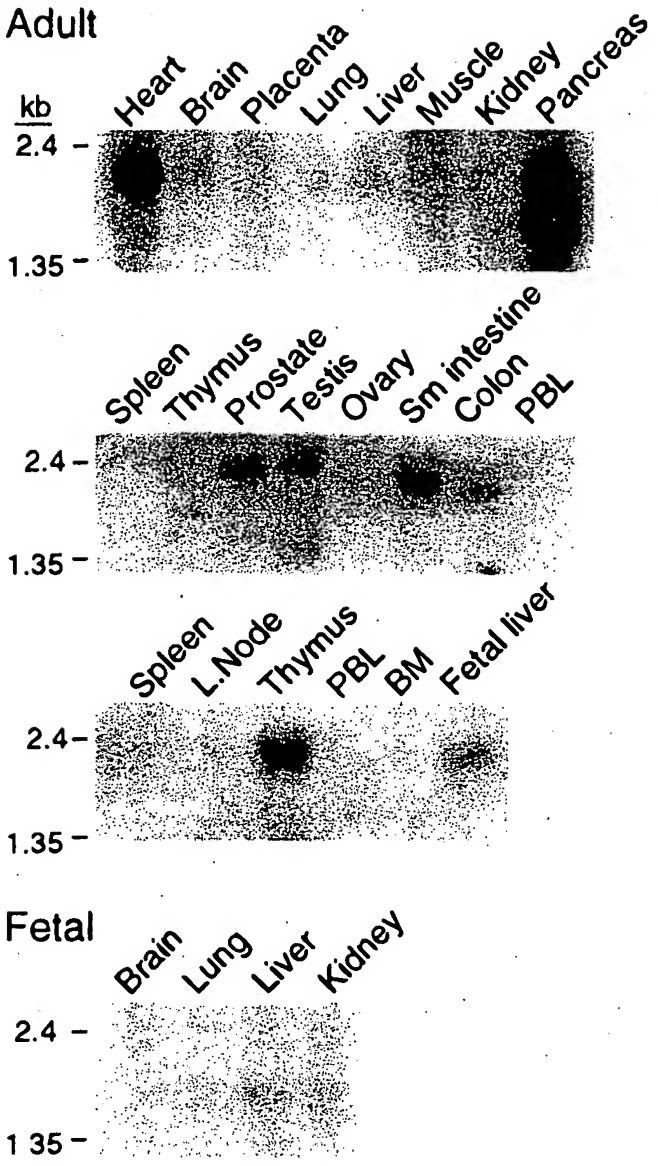

Adult
kb
2.4
1.35
Heart
Brain
Placenta
Lung
Liver
Muscle
Kidney
Pancreas
Spleen
Thymus
Prostate
Testis
Ovary
Sm intestine
Colon
PBL
2.4
1.35
Spleen
L.Node
Thymus
PBL
BM
Fetal liver
2.4
1.35
Fetal
Brain
Lung
Liver
Kidney
2.4
1 35

FIG. 7

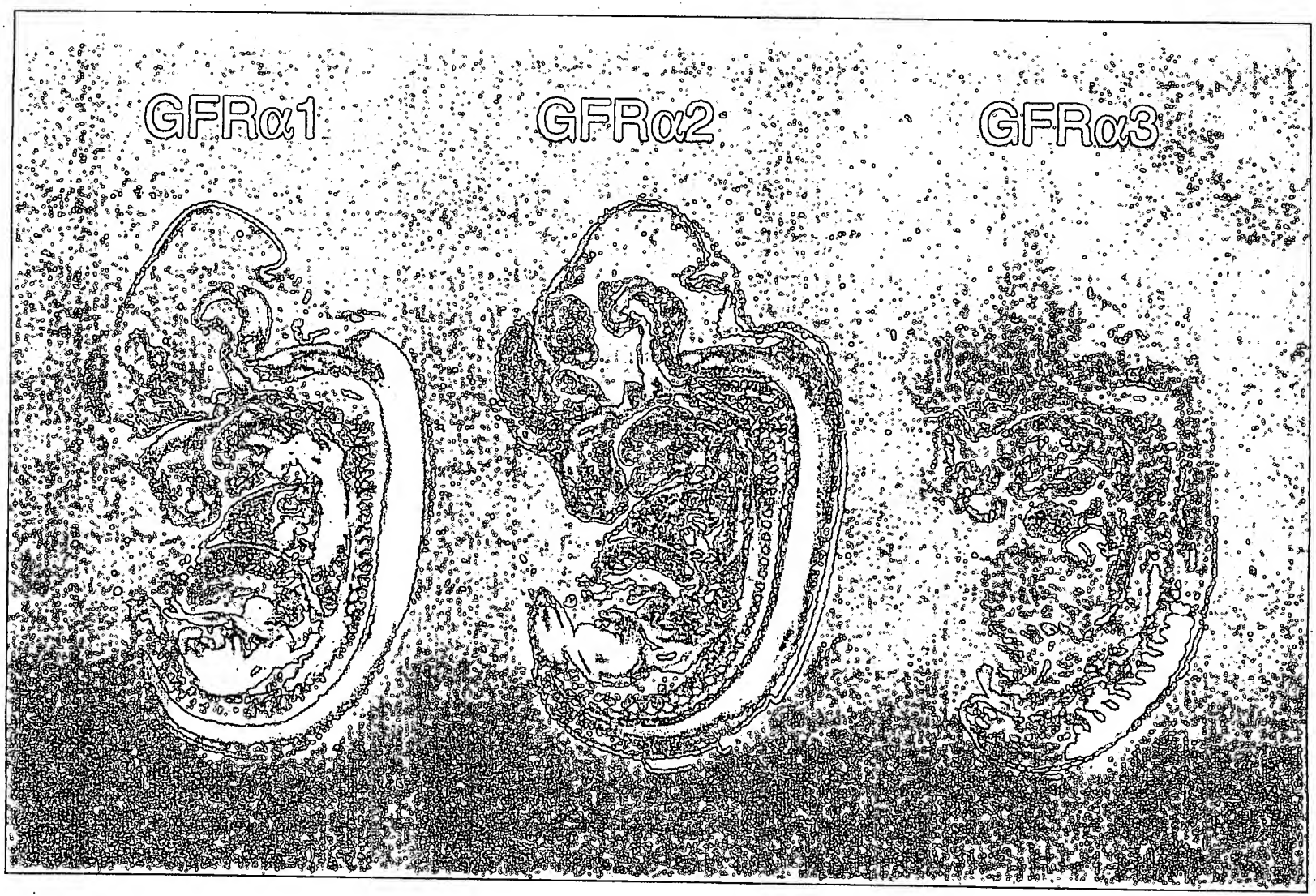


FIG. 8

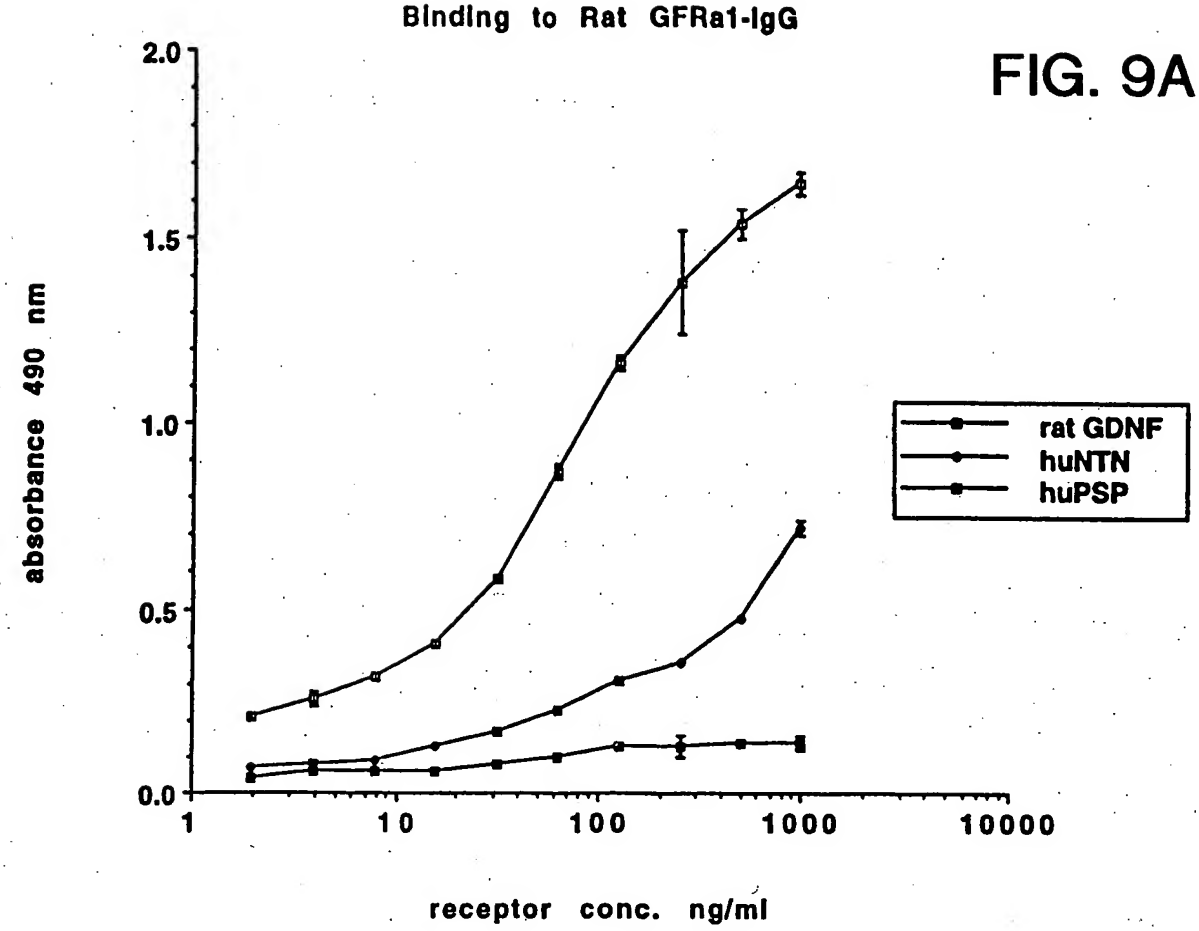

Binding to Rat GFRa1-IgG
absorbance 490 nm
2.0
1.5
1.0
0.5
0.0
1
10
100
1000
10000
receptor conc. ng/ml
rat GDNF
huNTN
huPSP

FIG. 9A

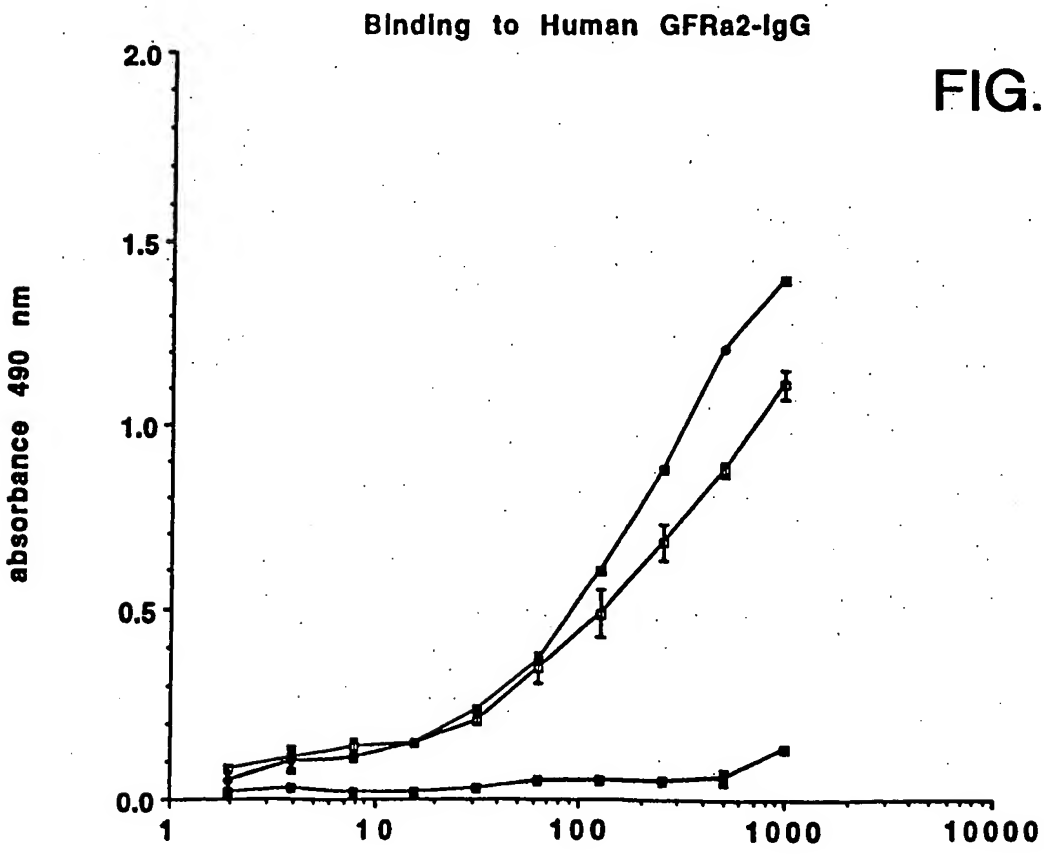

Binding to Human GFRa2-IgG
absorbance 490 nm
2.0
1.5
1.0
0.5
0.0
1
10
100
1000
10000

FIG. 9B

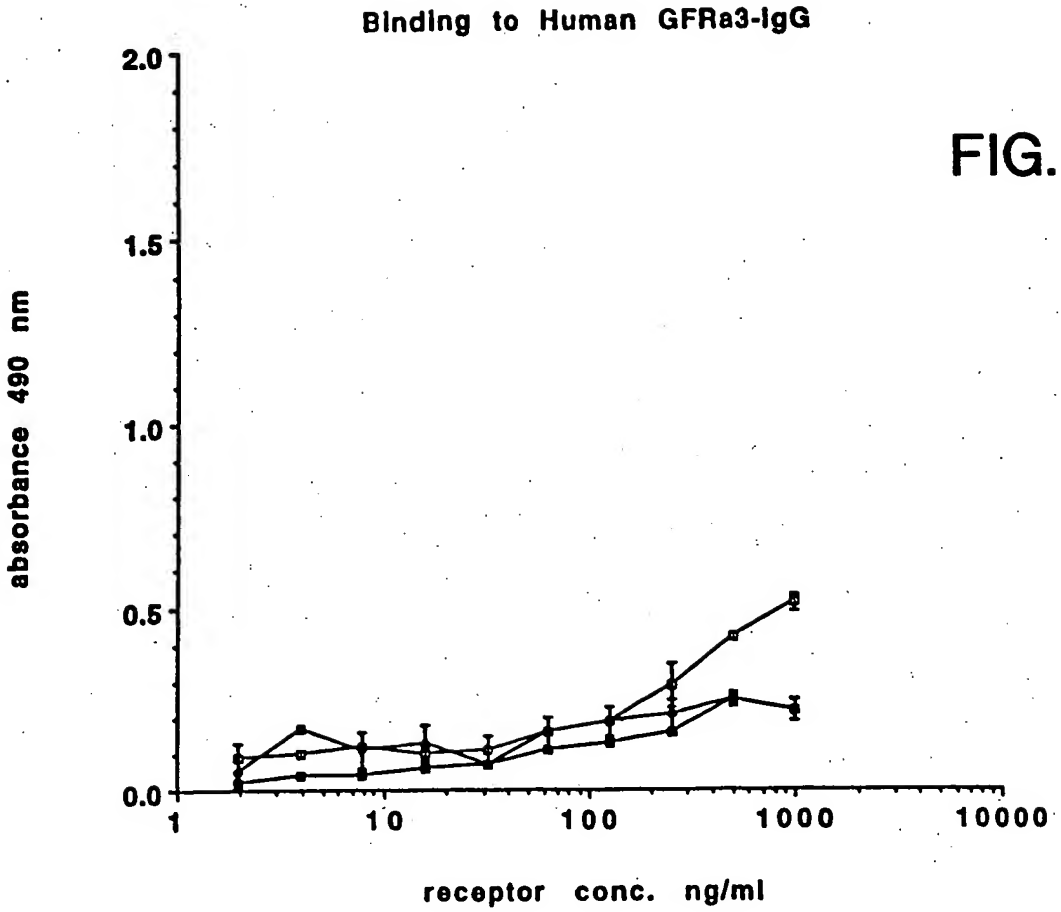

Binding to Human GFRa3-IgG
absorbance 490 nm
2.0
1.5
1.0
0.5
0.0
1
10
100
1000
10000
receptor conc. ng/ml

FIG. 9C

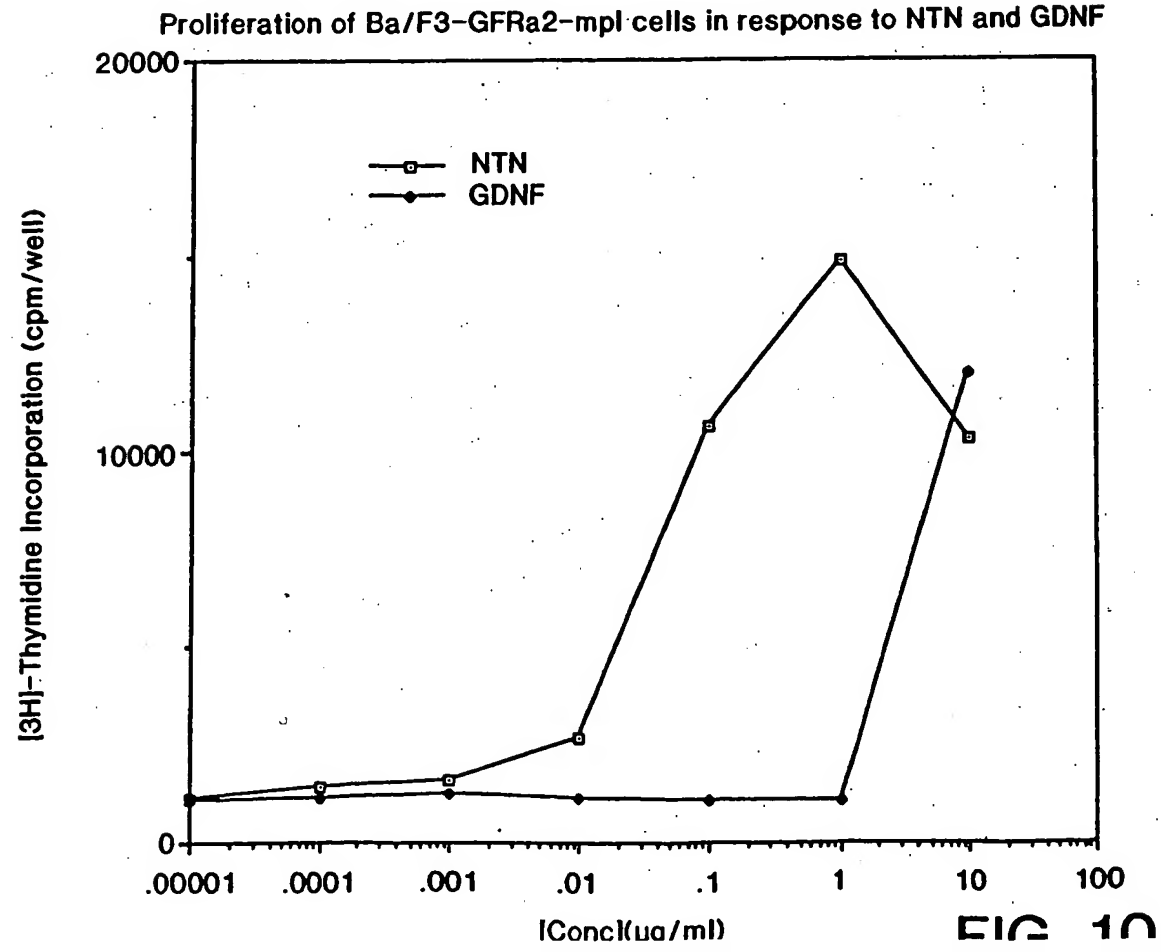

Proliferation of Ba/F3-GFRa2-mpl cells in response to NTN and GDNF
[3H]-Thymidine Incorporation (cpm/well)
20000
10000
0
NTN
GDNF
.00001
.0001
.001
.01
.1
1
10
100
[Conc](ug/ml)

FIG. 10

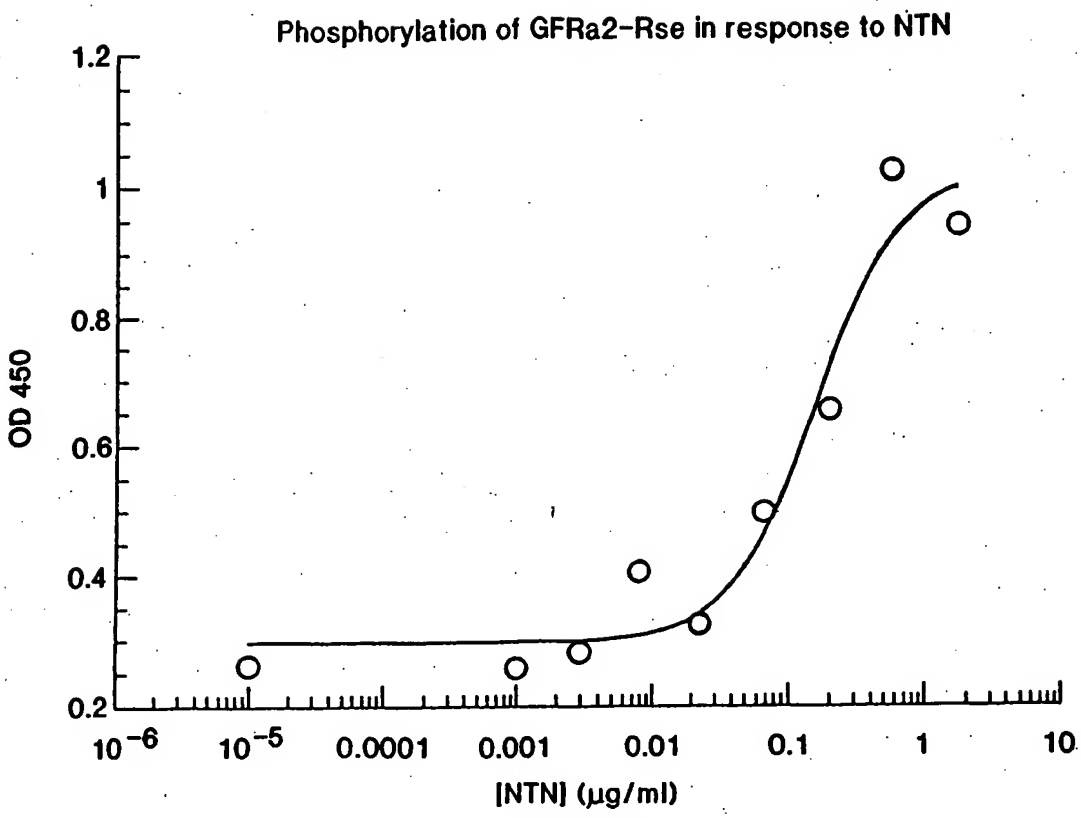

Phosphorylation of GFRa2-Rse in response to NTN
OD 450
1.2
1
0.8
0.6
0.4
0.2
10^{-6}
10^{-5}
0.0001
0.001
0.01
0.1
1
10
[NTN] (µg/ml)

FIG. 11

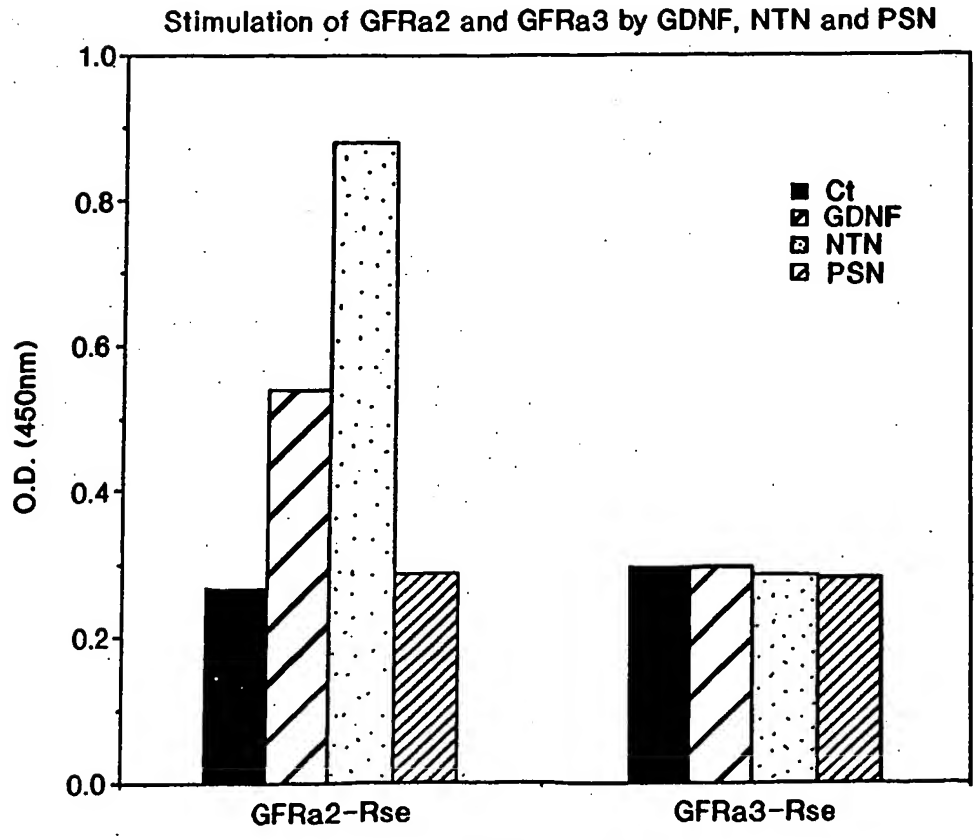
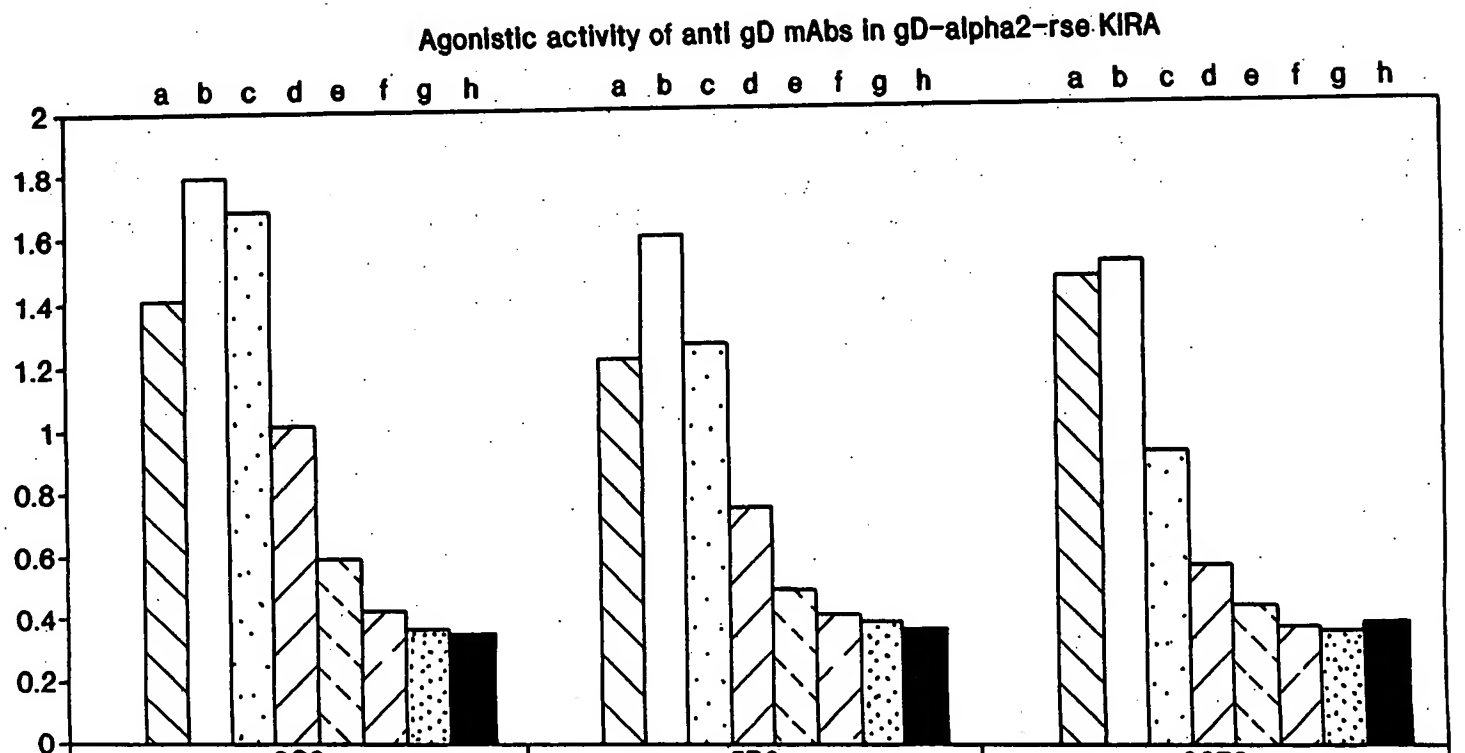

Stimulation of GFRa2 and GFRa3 by GDNF, NTN and PSN
O.D. (450nm)
1.0
0.8
0.6
0.4
0.2
0.0
Ct
GDNF
NTN
PSN
GFRa2-Rse
GFRa3-Rse

FIG. 12



	ug/ml	3C8	5B6	2272
a	1	1.409	1.211	1.463
b	0.4	1.791	1.600	1.511
c	0.16	1.684	1.267	0.915
d	0.064	1.017	0.749	0.562
e	0.0256	0.589	0.490	0.439
f	0.01024	0.427	0.406	0.371
g	0.004096	0.370	0.392	0.363
h	0	0.357	0.369	0.372

FIG. 13

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